



Steven M. Ruben
Appl. No. 10/662,429

Department	3
Subject	
Name	LILY X 10/14
Address	
National "Grand"	
Computation Notebook	
11 3/4" x 9 1/4", 4 x 4 Quad., 75 Sheets	43-648
	
0 73333 43648 a	
 AVERY DENNISON	
Office Products Chicopee, MA 01022	

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Ruben EXHIBIT #129

Department _____ 3

Subject _____

Name _____ CITY X-100

Address _____

National Brand

Computation Notebook

11 1/4" x 9 1/4", 4 x 4 Quad., 75 Sheets

43-648



0 73333 43648 8



AVERT
DENNISON

Office Products
Chicopee, MA 01022

Ruben EXHIBIT 2129
Ruben v. Wiley et al.
Interference No. 105,077
RX 2129

2-8-96 Test 00. for construct prior

4616 Trail HindIII 3'
 4617 " BamHI 5'
 4618 " BamHI 5'
 4619 HT4 HindIII 3'
 4620 " BamHI 5'
 4621 HoFMBo9 BamHI 5'
 4622 " Dsp718 3'

Sample ID	abs 260.0 nm	abs 280.0 nm	260.0 nm 280.0 nm	280.0 nm 260.0 nm	1=500
1 4616	0.0515	0.0330	1.5821	0.6402	0.9
2 4617	0.0400	0.0278	1.4471	0.6910	0.7
3 4618	0.0394	0.0260	1.5128	0.8811	0.6
4 4619	0.0484	0.0326	1.4830	0.6743	0.8
5 4620	0.0445	0.0291	1.5301	0.6536	0.7
6 4621	0.0613	0.0374	1.6401	0.6097	1
7 4622	0.0550	0.0391	1.4065	0.7110	0.9

PCR for construct:

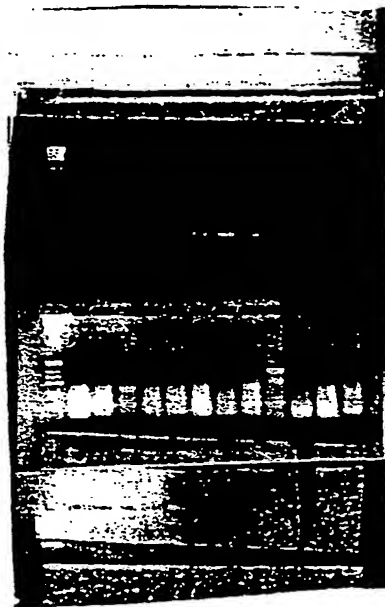
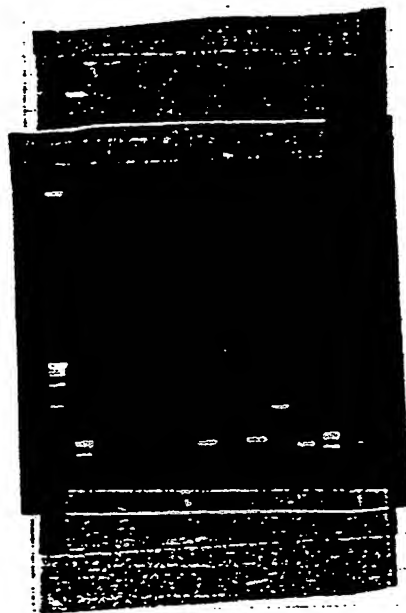
		Enzyme	Vector
1 HCACu62	4319+4320 3'	BamHI + ^{Dsp718} 41	pAZ
2 HCACu62	4319+14351 3'	" BamHI "	cHA
3 HTPA (Trail)	4616+4617 5'	HindIII + BamHI	pQE9
4 HTPA (Trail)	4616+4618 5'	HindIII + BamHI	pQE9
5 HT4	4619+4620 5'	HindIII + BamHI	pQE9
6 HoFMBo9	4621+4622 3'	BamHI + Dsp718	pAZ
7 HTTBN61	4577+4578 3'	BamHI + XbaI	Az-GP

2-8-96

PCR: for HITT B261

use T3 primer + 4579 primer

Take and Running 3% agarose gel for Southern Blot.



- | | |
|---------------|-----------|
| (1) H1QA | (17) H1K1 |
| (2) H1GX | (18) H1K2 |
| (3) HF | (19) HFS |
| (4) HBM | (20) HMF |
| (5) F. Brain | (21) HMA |
| (6) Hela | (22) HMA |
| (7) pinv. loc | (23) HMA |
| (8) HCE | (24) LV |
| (9) HET | (25) Hela |
| (10) HOF | |
| (11) HPL | |
| (12) HTA | |
| (13) HES | |
| (14) HLT | |
| (15) HPD | |
| (16) H50B | |

- Denature Buffer

labeling HITT B261 B261 specific primer = Buffer.

See
 oligo
 labeling

1 μ	(1 μ g) HITT B261 primer
5 μ	10x T4 PAK Buffer
1 μ	T-32p ATP
1 μ	T4 Kinase Enzyme (PAK)

42 μ H₂O

37°C 30'

add 10 μ g of spiner DNA 100ml
5m NaPO₄ PTC(control: 1X10⁸/200ml.

primer B261

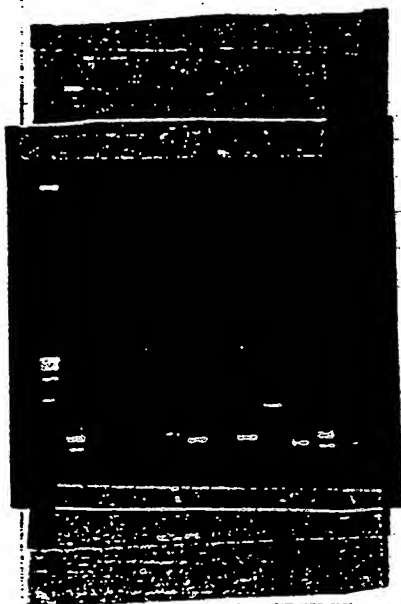
2/9/96

2-8-96

PCR: for HTTB61

use T₃ primer + 4579 primer

Take 5ml Running 3% agarose gel for Southern Blot.



- | | |
|--------------|---------|
| ① HLQA | ①7 HIK |
| ② HLQX | ①8 HXL |
| ③ HF | ①9 HFS |
| ④ HBM | ②0 HMF |
| ⑤ F. Brain | ②1 L |
| ⑥ Hela | ②2 HMA |
| ⑦ pinv. 1.2k | ②3 HTXA |
| ⑧ HCE | ②4 LV |
| ⑨ HET | ②5 Hda |
| ⑩ HAF | |
| ⑪ HPL | |
| ⑫ HTX | |
| ⑬ HES | |
| ⑭ HUH | |
| ⑮ HPD | |
| ⑯ HSOB | |

- Denaturation Buffer

Take the gel put in 300ml Denaturation Buffer.
at RT 1 hr

= Neutralization Buffer

300ml. shake the gel at RT. about 30'

= crosslink transfer. % weekend

- make oligo probe: use HTTB61 (4577) primer. B-HI

(conter: 1×10^8 / 200ml.

2/9/96

2-9-96

PCR for construct

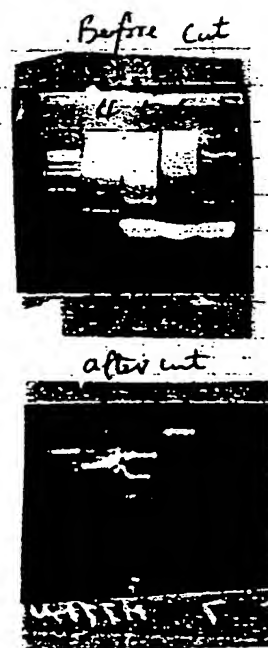
Running 2% low melting gel:

- (7) HIKI
 (14) HKL
 (14) HFS
 (12) LMG
 (21) LV
 (22) HHMA
 (23) HTA
 (24) LV
 (25) H2A

- (NKEF)
 1 HcAcub2
 (NKEF)
 2 HcAcub2
 (Fas L)
 3 HTPA



- (Fas L)
 4 HTPA
 (Fas Like)
 5 HT4
 6 HOFMB-9
 (TnFR)
 7 HTTBW61



at 70°C 10'
 phenol / ϕ X 3
 EtOH ppt (o/w method)

2-12-96 Digestion by SmaI

at 37°C incubate 2 hrs

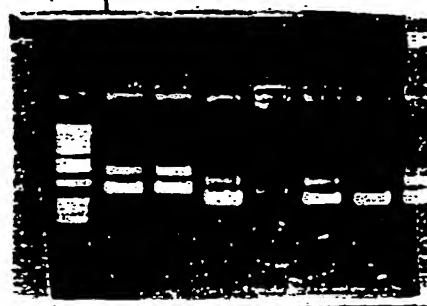
↓ phenol / ϕ X 3

↓ EtOH ppt

30 λ 15 λ 3 λ 1 λ 1 λ DLA + H₂OH₂ Buffer

BamHI XbaI

HindIII Asp211

Take 3 λ of each sample Run on gels

121

2-12-96

CSG7
~~CSG~~ Submit CSG16 for sequencing
 Hpp012
 use pQE 3' + 5' primer

2-12-96

Ligation to vector.

- | | | |
|----|---------|-------|
| #1 | HCAQub2 | pA2 |
| 2 | ... | CHO |
| 3 | HTPA | pQE9 |
| 4 | HTPA | pQE9 |
| 5 | HT4 | pQE9 |
| 6 | HOFMB09 | pA2 |
| 7 | H77B2b1 | A2-GP |

2-13-96

transformation to XL1Blue cell

2ul to 100ul XL1Blue cell
 on ice 15'
 42°C 1' add 1ml LB.
 37°C 1hr

pour plates 500 λ (LB+amp plate)

2-14-96

~~submit for sequencing:~~

CSG

Wash Southern Blot at RT 3 time
 exp. 4 hrs

2-14-96 pick up single clones to 100ml LB+amp
make PCR reactions:



grow up DNA

- #2 - 12
- #3 - 8
- #7 - 1

2-15-96 all constructed PCR primer use vector primer
made DNA prep:

BECKMAN DU-600

Date:

Nucleic Acid
Load Samples Method

MTA
MTA
MTA

2.6
1.5330 2.5
1.0075 0.5532 2.5

124

2-14-96 pickup 12 clone from HTTBW61 PCR products

use Eulglanal Buffer ppt.

-Clon: add 100ul Eulglanal Buffer

at RT 10'

centrifuge 10'

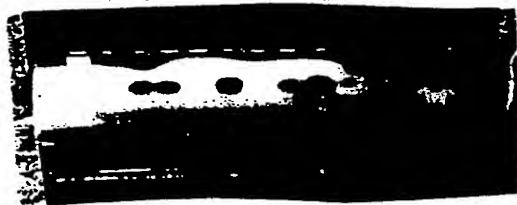
70% EtOH wash

Resuspend in 10ul of H₂O

Running on the gel to check the DNA

Submit for sequencing.

primer use HTTBW61 RPR3



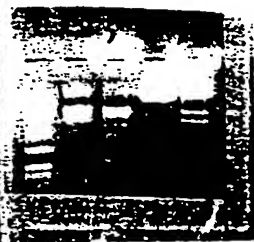
1-8 10-12 use 4ul of DNA

#9 use 1ul of DNA.

2-15-96

Digestio:

HCH2W62			HTPA			HTTBW61		
11K	un	cut	un	cut	un	cut	un	cut
	2			3		3		3



2-15-96

ligation again

#1	HeAcub2	PA2
#3	HTPA (Trail)	pQE9
#4	HTPA (Trail)	pQE9
#5	HT4	pQE9
#6	HoFmB09	PA2
#7	HTTB061	A2-GP

201

3 λ	DNA insert
3 λ	vector
4 λ	5x Ligation buffer
1 λ	T4 DNA ligase
9 λ	H ₂ O

RT 3.5 hrs

2-16

PCR for construction : primer Enzyme Vector

- ① HSABH13 4335 + 4336 ~~BamHI + Asp718~~ PA2
- ② HTXE133 4292 + 4293 ~~BamHI + Asp718~~ PA2
- ③ HoFmB09 4621 + 4622 ~~BamHI + Asp718~~ PA2
- ④ HTTB061 4577 + 4578 ~~BamHI + XbaI~~ A2-GP
- ⑤ HPDD012 4581 + 4582 ~~BamHI + HindIII~~ pQE9
- ⑥ HTPA (Trail) 4616 + 4617 ~~HindIII + BamHI~~ pQE9
- (first sequencing primer)
(HTPA1) ← ⑦ HTPA (Trail) 4616 + 4654 ~~BamHI + Asp718~~ pQE9
- ⑧ HT4 4619 + 4620 ~~HindIII + BamHI~~ pQE9
- ⑨ FASL 4657 + 4658 ~~HindIII + BamHI~~ pQE9
(HTF0016)

2/20/96

2-20-96 Running 2% low melting gel: (for construction)

cut down insert 70c 10'

phenol / ϕ x 3

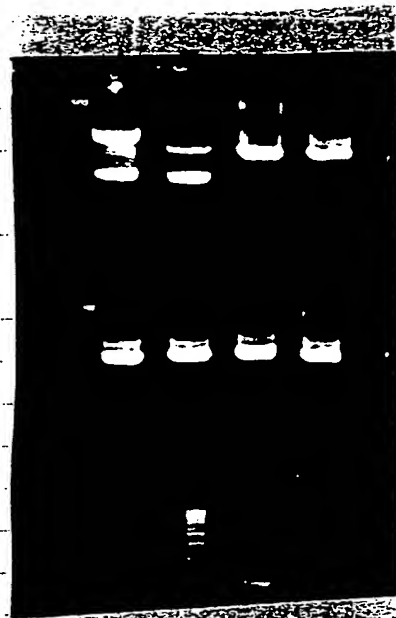
EtOH ppt 0/N



2-21-96 resuspend pellet in 25 λ H₂O

Digestion by Enzymes

	30 λ
DNA + H ₂ O	25 λ
B. Buffer	3 λ
Enzyme	1 λ
	1 λ



See 2/16/96

37°C incubate 2 hrs SmaI + BspI at 25°C incubate

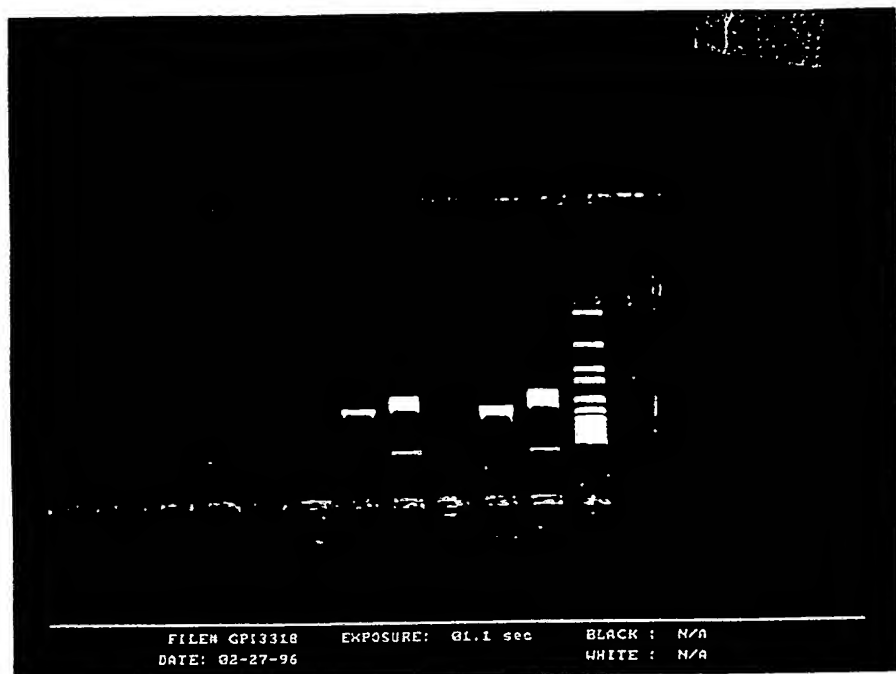
↓ after 2 hrs Take 3 λ of each sample Running on the gel:



vector

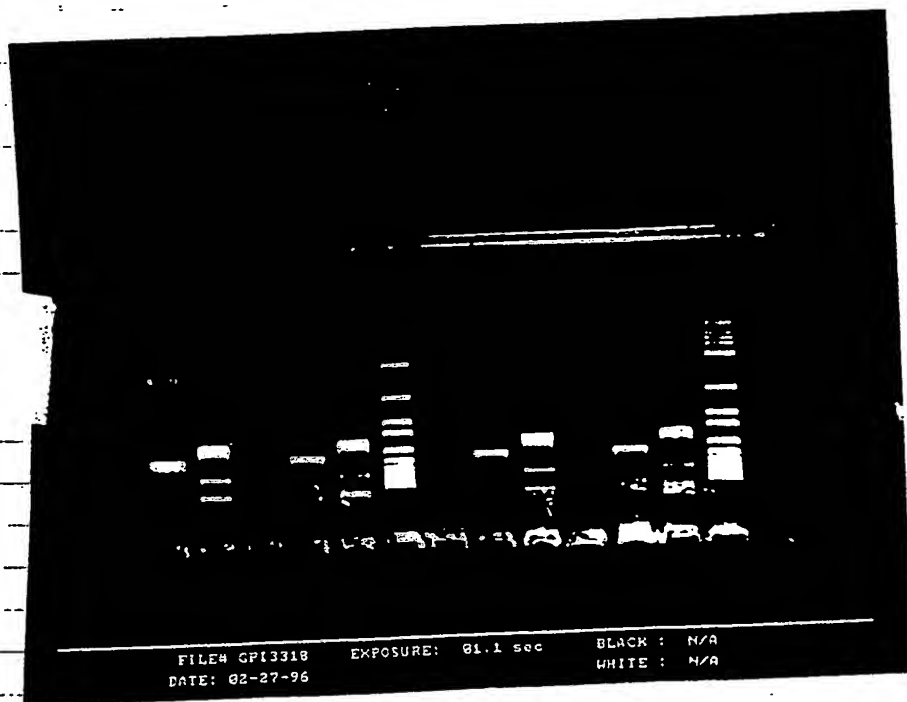
2-20-96 Running 2% low melting gel: (for construct)

in buffer. Invert. 75°C. 10'



5°C incubate

after 2 hrs Take 3x of each sample Running on the gel:



2-21-96 Digestion p₂9 vectors

cut by BamHI + HindIII

2/16/96

Take 5ul Running gel



p₂9

BamHI + HindIII

2-22-96 PCR for construction See pag 125

100ul PCR pr

150ul Promega Buffer (direct purification Buffer)

1ml PCR p₂9s DNA purification Resin

at RT incubate 2' pass column

80% isopropanol wash x2

50ul H₂O

Take 5ul Running on the gel.



Take 5ul digestion by enzymes:

after digestion: phenol x3 EtOH ppt. resuspend in 10ul H₂O

Ligation into vecto:

10ul	
2ul	Ligation Buffer
1ul	vector
6ul	DNA
1ul	T4 DNA Ligase
RT	5hrs

2-23-96 PCR:

#4 HTRN61 — use pA2 3' + 5' vector primer

#5 — use pA2 3' + 5' vector primer
#6 clone:
#3 #5 #9 #14

#2 #3

#1 #2

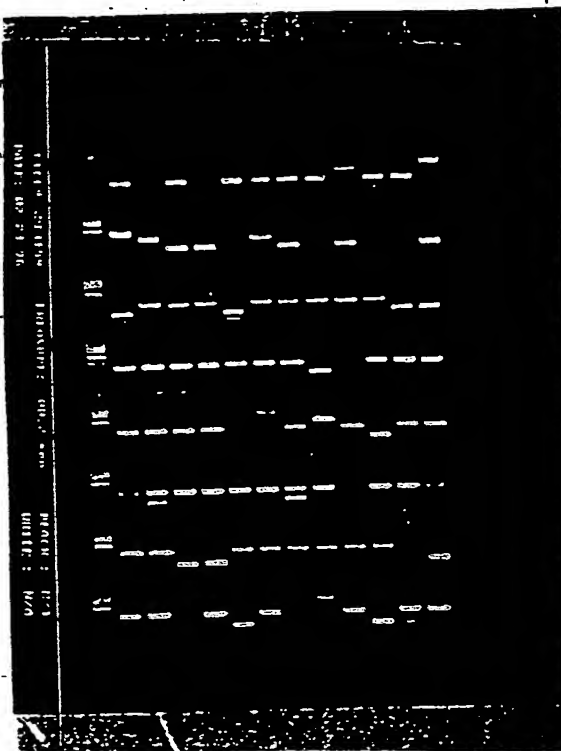
#1 #2

4

5

6

7



2-25-96 grow up DAA

2-26-96 make DAA prep:

Sample	abs	abs	260.0 nm	280.0 nm
13	260.0 nm	280.0 nm	280.0 nm	260.0 nm
4-3	0.2317	0.1364	1.6990	0.5886
4-5	0.1649	0.0933	1.7679	0.5656
4-7	0.0704	0.0403	1.7461	0.5727
4-14	0.0805	0.0427	1.8850	0.5305
5-2	0.0536	0.0271	1.3729	0.5069
5-3	0.0877	0.0472	1.8594	0.5378
6-1	0.0730	0.0381	1.9152	0.5221
6-2	0.0651	0.0338	1.9188	0.5212
7-1	0.0798	0.0415	1.9739	0.5198
7-2	0.1008	0.0532	1.8951	0.5277
11	0.0623	0.0383	1.6278	0.6144
12	0.0781	0.0474	1.6069	0.6223
13				

5.8

4.1

1.8

2.0

1.3

2.2

1.8

1.6

2.0

2.5

1.7

1.3

Submit for sequencing

HTRN61 use pA2 3' + 5'

HTRN62

HTRN

HTRN

2-26-96 PCR for construct.

#1 H5ABH13 > use pA23' + 5'
 #3 HOFMB09
 #8 HT4 — use pA25' + 3'

- PCR for CSG16 [15296 + 14813']

HTXE133 4293 + 4293

(HNF1016) FASL 4656 + 4657

NC01 + HindIII pA260

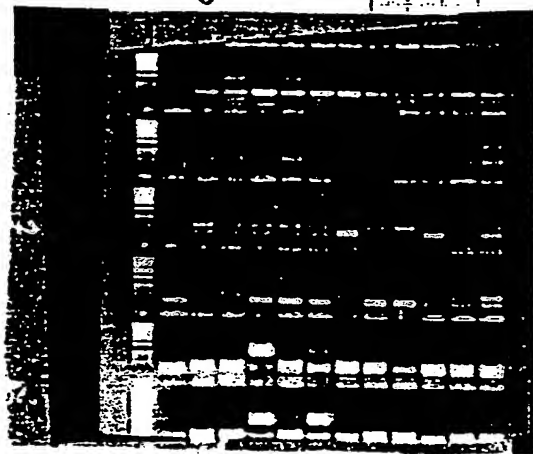
2-27-96

grow up DNA
 0/N

H5ABH13 ←
 #3 A20

HOFMB09 ←

HT4 ←
 #4 #16

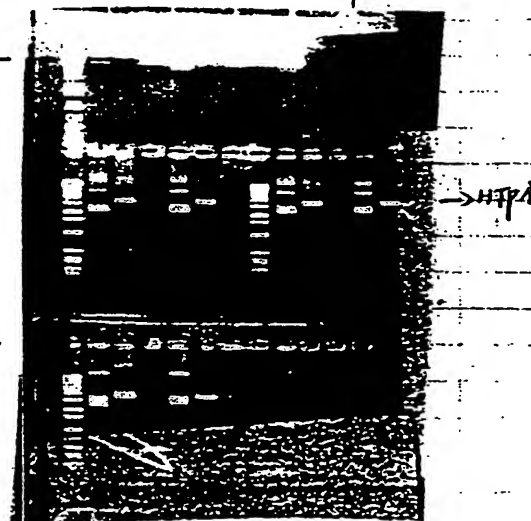


- Digest: 2/26/96 DNA prep. Running 1% agarose gel:

HTTBAB1 ←

HPO000012 ←

HTPA BsmH3 ←



2-26-96 PCR for construct.

#1 HSABH13 > use pA23+5'
 #3 HOFMB09
 #8 HT4 — use pA23+3'

- PCR for CSG16 [15296 + 14813]
 HTXEL33 4273 + 4273
 (HNF1016) FASL 4656 + 4657

this new CSG16 NCO15'
 primer.

NCO1 + HindIII pA260

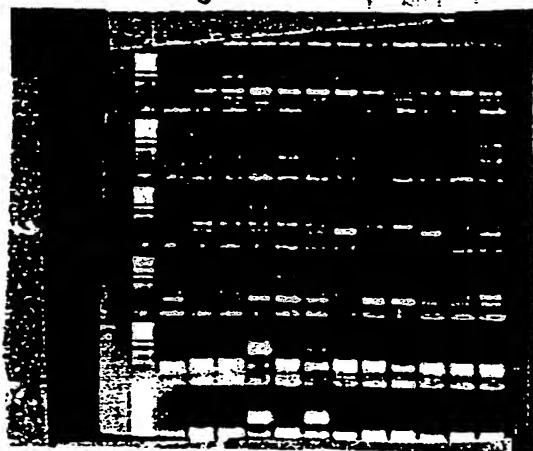
2-27-96

grow up on A
 O/N

HSABH13 ←
 #3 A20

HOFMB09 ←

HT4 ←
 #4 #16

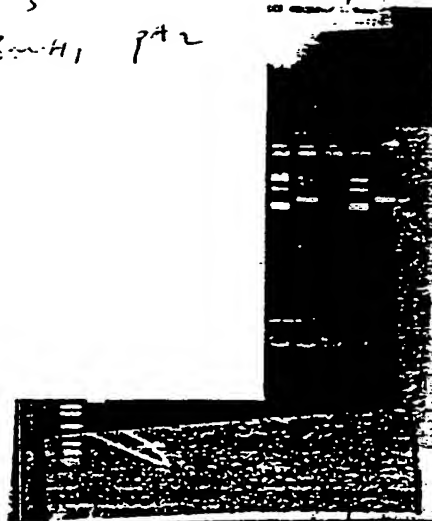


- Digestion 3/26/96 max prep. p.

5 3

HCAcub2 BamHI + BamHI pA2

gel:



HT4

130

2-27-96

2841	PAZ / A2GP 3'
1474	PAZ 5'
2785	A2GP 5'

2-28-96

Results file: A:\WORK_RES

Method name: A:\DEFAULT

Assay type: General Ratio and Concentration

Units: ug/ml

Formula setup: VIZW

Background Correction: (No)

Sampling device: One cell

Concentration: (No)

Read average time: 0.50 sec

Peak Pick: (No)

11 1:500

Sample ID	abs	abs		260.0 nm	280.0 nm	
				260.0 nm	260.0 nm	
1	5	0.3443	0.0233 HSAHA13	1.3006	0.5262	1.1
2	u	0.0736	0.0398 HTU	1.3498	0.5406	1.8
3						

2.4 out
in standard box

Submit for sequencing:

HSAHA13 #3 PAZ 3' + 5'
HTU #4 PAZ 3' + 5'

2-28-96

(4LH1HCS8) INTERCEPT full

Forward

Reverse

HTH1H61 RPR1
RPR3
RPR1
F3
R3
F4

RP02
R4
R5

Repeat sequencing

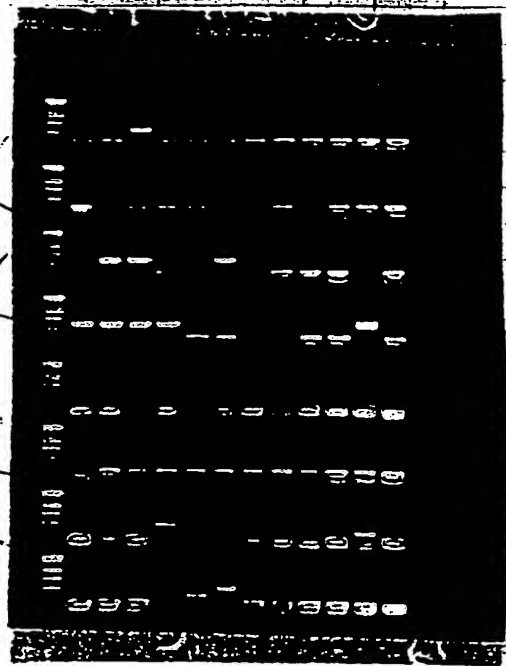
Reverse > add 1% DMSO
F3

2/2/96

2-27-96 PCR for HTXEL33 PAZ - use PAZ 3' + 5'
 HTTBV61 Az-GP → use PAZ 3' + AzGP 5'
 FASL (HNF1016) pRE9 pRE 3' + 5'
 CSG16 pRE6a

grow up DNA 5/11

HTXEL33
 pickup #3
 HTTBV61
 #2 #14
 FASL (HNF1016)
 CSG16
 #4 #16 #18



3/1/96 make DNA prepr:

Submit for sequencing:

HTXEL33 PAZ 3' + 5'
 HTTBV61 Az-GP 3' + 5'
 CSG16 pRE 3' + 5'

Submit HTTBV61 for sequencing

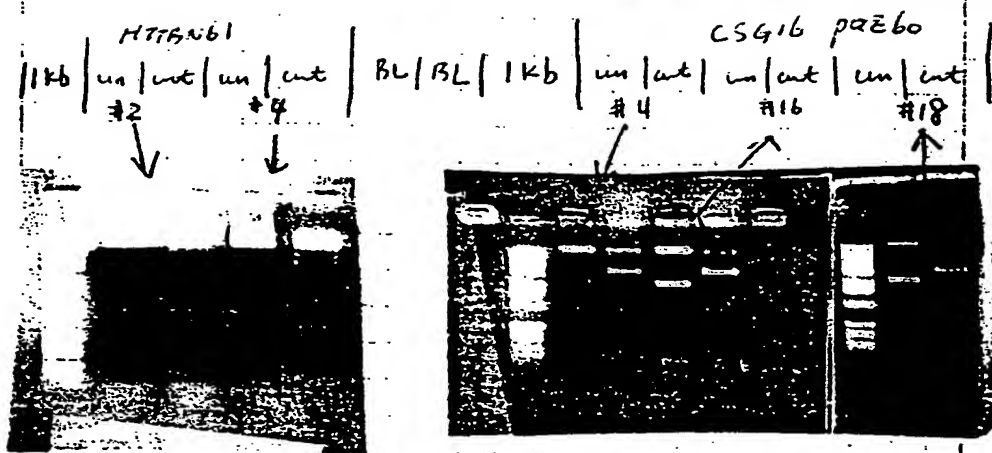
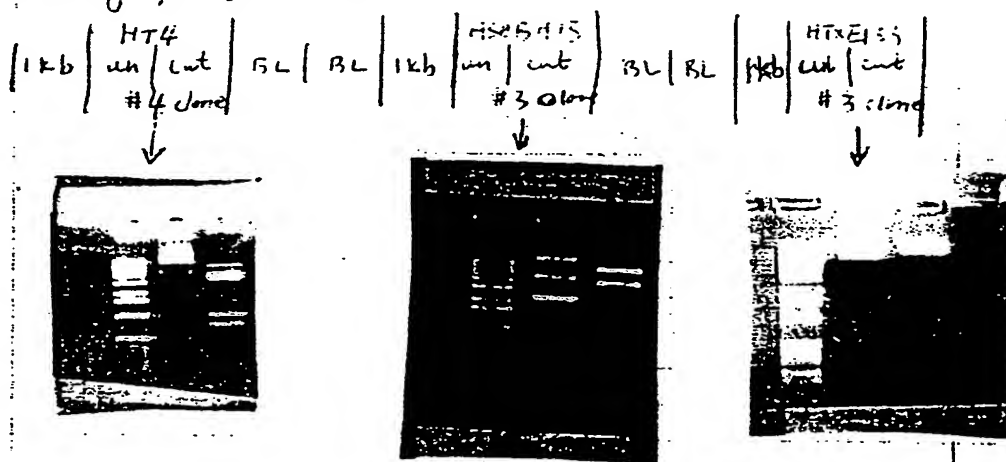
HLMERIS Reverse add 1% DMSO
 F3

Nucleic Acid	Method	SaveClear	Print	Q
ReadSamples				
Results file: A:\WORK_RES		Method name: A:\OUTFAMEL		
Assay type: General Ratio and Concentration		Units: ug/ml		
Formula setup: VIEW		Background Correction: (No)		
Sampling device: One cell		Concentration: (No)		
Read average time: 0.50 sec		Peak Pick: (No)		
Sample ID	abs 260.0 nm	abs 280.0 nm	260.0 nm / 280.0 nm	280.0 nm / 260.0 nm
1 HTXEL33	0.0438	0.0234 #3	1.8724	0.5341 1.1
2 HTTBV61	0.0794	0.0412 #2	1.9274	0.5188 1.2
3 HTTBV61	0.0443	0.0245 #14	1.8070	0.5534 1.1
4 CSG16	0.0171	0.0078 #4	2.1931	0.4560 1.1
5 CSG16	0.0358	0.0184 #16	1.9322	0.5176 1.1
6 CSG16	0.0244	0.0130 #18	1.8756	0.5332 1.1

5-4-76 Degradation DNA (See page 131)

			<u>Result</u>
(1) HT4	pAE9	BamHI + HindIII	B
(2) HSABH13	pA2	BamHI + Asp718	B
(3) HTXE133	pA2	SamI + Asp718	A
(4) HTTB61	A2-GP	BamHI + XbaI	A
(5) CSG16	pAE60	NcoI + HindIII	B

Running 1% agarose gel:



3-5-96

Digestion for HTBabi/A2-LP #9 done

cut 1/2.



Transformation to M15 cell.

HPO0012 #3 clone

HTPA003504 #2 clone (short)

HTPA003504 #2 clone (long)

HT4 (from ligation).

pour plate (LB+A+K)

3-6-96

grow up clones at LB+A+K medium
(for protein induction)

37°C 1/2.

grow up:

HPO0012 #3 1 — 4

HTPA (short) #2 5 — 8

HTPA (long) #2 9 — 12

CS46 14 — 15

CS47 16 — 17

3-7-96

take 30 µl to 3ml

LB+A+K

37°C 25 hrs

add 30 µl IPTG to 3ml

37°C 3 hrs

3-7-76 Take 800λ spin down. waste 1

add 15λ of H₂O
15λ of 50% loading buffer
mix well 5'

Running 10% SDS page:

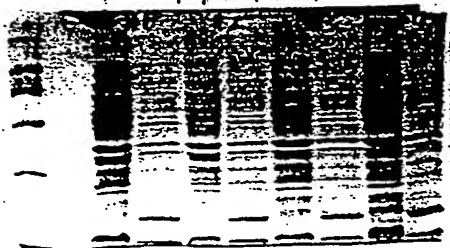
#1 gel: |m| 6L | 1 | 1⁺ | 2 | 2⁺ | 3 | 3⁺ | 4 | 4⁺ |

#2 gel: |m| 5 | 5⁺ | 6 | 6⁺ | 7 | 7⁺ | 8 | 8⁺ | 13L |

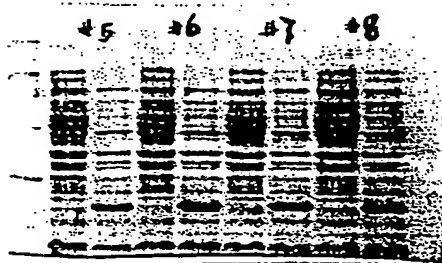
#3 gel: |m| 9 | 9⁺ | 10 | 10⁺ | 11 | 11⁺ | 13L | 12 | 12⁺ |

#4 gel: |m| 14 | 14⁺ | 13L | 15 | 15⁺ | 16 | 16⁺ | 17 | 17⁺ |

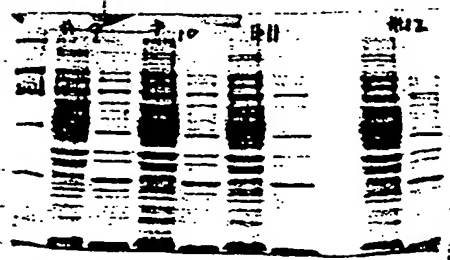
#1 H₂O 12 39 / 2000000000
pH 4.0 4.0 4.0 4.0 4.0 4.0



#2



H₂O (12-100) 12 / 2000000000
#3



CS46/p429 #4



CS47/p429

3-8-76 running H₂O 12 / p429 B₂H₄ + H₂O # 1 2 3 4
H₂O (12-100) / p429 B₂H₄ + H₂O # 5 6 7 8
H₂O (12-100) / p429 B₂H₄ + H₂O # 9 10 11 12

3-7-96 PCR for HT4 (conserved) in HT5 cell

use 4619 + 4620 specific primer. Total 36 clones

3-8-96 Running 1% agarose gel:

pick up #13 #15

(protein induction)



3-8-96 growing HT4 #13 #15 O/N

LB + A + K medium

3/14/96

→ Jim N: Title HPOD012 at
HTA4 - long at clone
HTA4 - short PI

3/3/96

3-11-96

protein induction

↓

late 30A to 3rd LB+ATK medium

↓ 37°C 2.5 hrs

↓ add 30A of IPTG (~~100~~)

↓ 37°C 3 hrs

Running 15% SDS page:

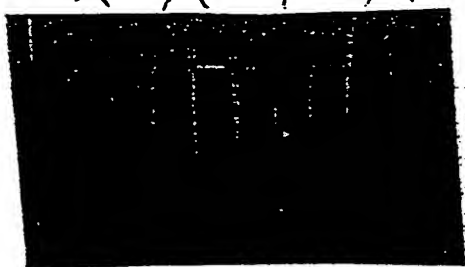
decabone not found?

CS416

HT4

CS416

CS417

- Repeat 3/21/96
gel~~that~~

Repeat

CS416

HT4 0072

> confirmed. See 3-11-96

5-11-96 PCR for CS616 $NcoI + BamHI$ / PA2

(HCCAT) + 2 \times CS616 15276 $NcoI$ 5' + 12121 $BamHI$ 3' (HCCAT) 72)

(1) CS616 15296 $NcoI$ 5' + 14883 $HindIII$ 3' (' ' ')

5-12-96 after PCR Take SA Running on the gel:

↓ Take 100 λ of PCR
100 λ Promega buffer (Kit)
1 ml PCR on a Resin
RT 1'

↓ pass column wash $\times 2$ 50% isopropanol

↓ add 100 λ of H₂O

↓ Take SA Running on the gel

digestion: Take 10 λ of PCR insert

5 λ of B-buffer

1 λ $NcoI$

1 λ $BamHI$

37° incubate 2 hrs

loading all sample on the gel:

↓ GeneScreen

↓ after GeneScreen
Running on the gel

after digestion Running on the gel



cut down insert

Digestion pRE60 $NcoI + BamHI$
after 0/12 Take SA Running on the gel



the only pool
in vector

3-13-76

H74 0.0152

Dezember 1841 + 1842

37°C = hrs

↓ phenol x 3

↓ checker x1

↓ ε_{TOH} $\rho\rho^t$

↓ resuspended in cold H₂O

— Liget: w: to p2E9 v2etoy (BarH₁ + Hind^{III})

- Transformation to new cell:

- 37°C %w

after per. p.m. font
 plate 7th line - 1000 g

3-14-96

PCR for CSG16 / pGE60

$$(15296 + 12121)$$
$$NCO + BaOH$$

HT 4472 / p² 29

$$\text{BaH}_2 + \text{Hind}^{\oplus} \text{Y}^-$$

use pQE3⁺ + 5' primer

pick up clone

CSG16

$$1 \quad 2 \quad 3 \quad 4$$

HT4 567-8

SUPERVISOR

DATE-

~~03/14/98~~

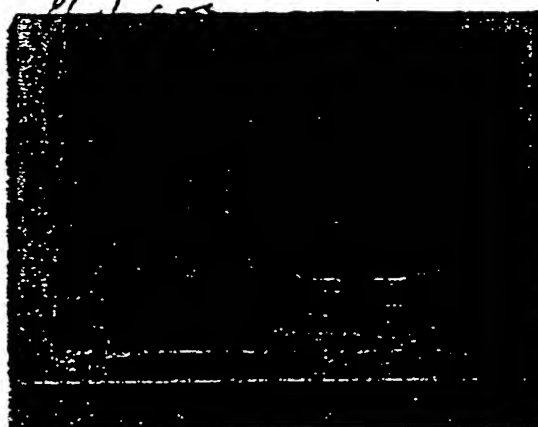
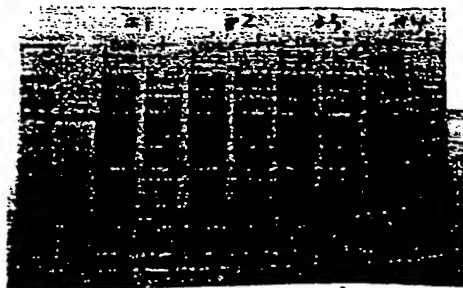
3-15-96 CS616 protein induction
HT4

CS616 1-4 clone
HT4 5-8 clone

#1 gel: |m| BL | 1 | 1 | 2 | 2 |

#2 gel: |m| 5 | 5 | 6 | 6 | 7 | 7 |

#1 gel: CS616/pAZ60



clone from
to Jim Ni
3/26/96

3-15-96 forcing go CS616/pAZ60 NcoI + BstHI #1 #2 clone
HT4/pAZ60 BstHI + HindIII #5 #6 #7 #8 clone

3-17-96 grow up CS616 #1, 2 clone for DLA
HT4/pAZ60 #5 #6

3-18-96 Do DLA prep: for CS616 #1, 2
HT4/pAZ60 #5, 6

Assay type: General Ratio and Concentration
Formula setup: VIEW
Sampling device: One cell
Read average time: 0.50 sec

Units: ug/ml
Background Correction: [No]
Concentration: [No]
Peak Pick: [No]

Sample ID	abs 260.0 nm	abs 280.0 nm	1.500	280.0 nm	280.0 nm
				280.0 nm	260.0 nm
1	CS616 #1	0.0406	0.0209	1.9434	0.5148
2	CS616 #2	0.0330	0.0176	1.8681	0.5353
3	HT4 #1	0.0754	0.0406	1.8585	0.5387
4	HT4 #6	0.0341	0.0161	2.1179	0.4722
5	HT4 #5	0.0656	0.0359	1.8287	0.5466
6	pAZ60				

1.4/λ
0.8/λ
1.8 - dist. - 0.9/λ
0.9
1.6

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